BIOTECHNOLOGY
SYSTEMS
BRANCH
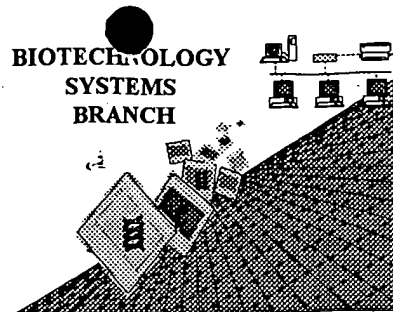
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/754,831*

Source: *O/PE*

Date Processed by STIC: *10/1/2001*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *09/754,831*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1_____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2_____Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length
Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>
Sequence(s) *44 and more* missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 10/01/2001
PATENT APPLICATION: US/09/754,831   TIME: 15:09:56

Input Set : A:\STK-008CN.txt
Output Set: N:\CRF3\10012001\I754831.raw

```
   3 <110> APPLICANT: Oppermann, Herman
   4         Kuberasampath, Thangavel
   5         Rueger, David
   6         Ozkaynak, Engin
   8 <120> TITLE OF INVENTION: Osteogenic Devices
  10 <130> FILE REFERENCE: STK-008CN
  12 <140> CURRENT APPLICATION NUMBER: US 09/754,831
  13 <141> CURRENT FILING DATE: 2001-09-10
  15 <150> PRIOR APPLICATION NUMBER: US 08/375,901
  16 <151> PRIOR FILING DATE: 1995-01-20
  18 <150> PRIOR APPLICATION NUMBER: US 08/145,812
  19 <151> PRIOR FILING DATE: 1993-11-01
  21 <150> PRIOR APPLICATION NUMBER: US 07/995,345
  22 <151> PRIOR FILING DATE: 1992-12-22
  24 <150> PRIOR APPLICATION NUMBER: US 07/315,342
  25 <151> PRIOR FILING DATE: 1989-02-23
  27 <150> PRIOR APPLICATION NUMBER: US 07/232,630
  28 <151> PRIOR FILING DATE: 1988-08-15
  30 <150> PRIOR APPLICATION NUMBER: US 07/179,406
  31 <151> PRIOR FILING DATE: 1988-04-08
  33 <160> NUMBER OF SEQ ID NOS: 72
  35 <170> SOFTWARE: PatentIn version 3.0
```

Does Not Comply
Corrected Diskette Needed

OK-> (annotation on line 13)

ERRORED SEQUENCES

```
1935 <210> SEQ ID NO: 45
1936 <211> LENGTH: 4
1937 <212> TYPE: PRT
1938 <213> ORGANISM: Artificial Sequence
1940 <220> FEATURE:
1941 <223> OTHER INFORMATION: Hinge region
1943 <400> SEQUENCE: 45
1945 Asp Pro Asn Gly
1946 1                    ⟶ delete
2376 <210> SEQ ID NO: 58
2377 <211> LENGTH: 15
2378 <212> TYPE: PRT
2379 <213> ORGANISM: Artificial Sequence
2381 <220> FEATURE:
2382 <223> OTHER INFORMATION: inhibin
2384 <400> SEQUENCE: (49) 58
2386 Gly Tyr His Ala Asn Tyr Cys Glu Gly Glu Cys Pro Ser His Ile
2387 1               5                   10                  15
2508 <210> SEQ ID NO: 67
2509 <211> LENGTH: 5
2510 <212> TYPE: PRT        P.2
```

E--> (annotation on line 1946)
E--> (annotation on line 2384)

RAW SEQUENCE LISTING   DATE: 10/01/2001
PATENT APPLICATION: US/09/754,831   TIME: 15:09:56

          Input Set : A:\STK-008CN.txt
          Output Set: N:\CRF3\10012001\I754831.raw

```
     2511 <213> ORGANISM: Artificial Sequence
     2513 <220> FEATURE:
     2514 <223> OTHER INFORMATION: Vg1
E--> 2516 <400> SEQUENCE: (57) 67
     2518 Leu Tyr Val Glu Phe
     2519 1                 5
     2574 <210> SEQ ID NO: 72
     2575 <211> LENGTH: 5
     2576 <212> TYPE: PRT
     2577 <213> ORGANISM: Artificial Sequence
     2579 <220> FEATURE:
     2580 <223> OTHER INFORMATION: N-terminal sequence
     2582 <400> SEQUENCE: 72
     2584 Cys Lys Arg His Glu
     2585 1                 5
E--> 2586 (1) delete
E--> 2589 (2) delete
```

see next page

```
<210>  44
<211>  102
<212>  PRT
<213>  Artificial Sequence      see item 11 on Erra summary sheet
<400>  44
```

Asp Pro Asn Gly Leu Tyr Val Asp Phe Gln Arg Asp Val Gly Trp Asp
1   5   10   15

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

FYI Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

Input Set : A:\STK-008CN.txt
Output Set: N:\CRF3\10012001\I754831.raw

```
L:13  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:107 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:115 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:118 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:121 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:124 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:127 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:130 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:147 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:152 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:155 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:158 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:161 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:164 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:167 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:170 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:521 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:524 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:527 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:530 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:533 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:536 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:923 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:926 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:929 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
```

Input Set : **A:\STK-008CN.txt**
Output Set: **N:\CRF3\10012001\I754831.raw**

```
L:929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:932 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:935 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:938 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:941 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:941 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1444 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1462 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1480 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:1480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1501 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:1501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1537 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:1561 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:1561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:1579 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
L:1579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1582 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
L:1582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1600 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:1600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1603 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:1603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1906 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1906 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1946 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:2164 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:2164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2262 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2262 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2384 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:58 differs:49
L:2516 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:67 differs:57
L:2586 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:72
M:332 Repeated in SeqNo=72
```